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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=7; day=31; hr=13; min=14; sec=29; ms=661; ]

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Application No: 10588052 Version No: 2.0

**Input Set:****Output Set:**

**Started:** 2008-07-25 21:59:02.447  
**Finished:** 2008-07-25 21:59:05.030  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 583 ms  
**Total Warnings:** 30  
**Total Errors:** 1  
**No. of SeqIDs Defined:** 83  
**Actual SeqID Count:** 83

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (22)
W 402	Undefined organism found in <213> in SEQ ID (24)
W 402	Undefined organism found in <213> in SEQ ID (27)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (38)
W 402	Undefined organism found in <213> in SEQ ID (41)
W 402	Undefined organism found in <213> in SEQ ID (43)
W 402	Undefined organism found in <213> in SEQ ID (46)

**Input Set:**

**Output Set:**

**Started:** 2008-07-25 21:59:02.447  
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**Total Warnings:** 30  
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**No. of SeqIDs Defined:** 83  
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Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (48)
W 402	Undefined organism found in <213> in SEQ ID (49)
W 402	Undefined organism found in <213> in SEQ ID (57)
W 402	Undefined organism found in <213> in SEQ ID (60)
W 402	Undefined organism found in <213> in SEQ ID (62)
W 402	Undefined organism found in <213> in SEQ ID (65)
W 402	Undefined organism found in <213> in SEQ ID (67)
	This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> KIM, DO-MAN  
KANG, HEE-KYOUNG  
LEE, JIN-HA

<120> PROTEIN WITH ACTIVITY OF HYDROLYZING AMYLOPECTIN, STARCH,  
GLYCOGEN AND AMYLOSE, GENE ENCODING THE SAME, CELL EXPRESSING THE  
SAME, AND PRODUCTION METHOD THEREOF

<130> 44352-0011-00US

<140> 10588052  
<141> 2006-07-31

<150> PCT/KR05/00235  
<151> 2005-01-27

<150> KR 10-2004-0006186  
<151> 2004-01-30

<160> 83

<170> PatentIn version 3.3

<210> 1  
<211> 647  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
polypeptide

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20 25 30  
  
Val Thr Val Leu Ser Ser Pro Glu Ser Val Thr Ser Ser Asn His Val  
35 40 45  
  
Gln Leu Ala Ser His Glu Met Cys Asp Ser Thr Leu Ser Ala Ser Leu  
50 55 60  
  
Tyr Ile Tyr Asn Asp Asp Tyr Asp Lys Ile Val Thr Leu Tyr Tyr Leu  
65 70 75 80  
  
Thr Ser Ser Gly Thr Thr Gly Ser Val Thr Ala Ser Tyr Ser Ser Ser

					85						90						95	
Leu	Ser	Asn	Asn	Trp	Glu	Leu	Trp	Ser	Leu	Ser	Ala	Pro	Ala	Ala	Asp			
					100						105						110	
Ala	Val	Glu	Ile	Thr	Gly	Ala	Ser	Tyr	Val	Asp	Ser	Asp	Ala	Ser	Ala			
					115						120						125	
Thr	Tyr	Ala	Thr	Ser	Phe	Asp	Ile	Pro	Leu	Thr	Thr	Thr	Thr	Thr	Ser			
					130						135						140	
Ser	Ser	Ser	Ala	Ser	Ala	Thr	Ser	Thr	Ser	Ser	Leu	Thr	Thr	Thr	Ser			
145						150						155						160
Ser	Val	Ser	Ile	Ser	Val	Ser	Val	Pro	Thr	Gly	Thr	Ala	Ala	Asn	Trp			
					165						170						175	
Arg	Gly	Arg	Ala	Ile	Tyr	Gln	Ile	Val	Thr	Asp	Arg	Phe	Ala	Arg	Thr			
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Asp	Gly	Ser	Thr	Thr	Tyr	Leu	Cys	Asp	Val	Thr	Asp	Arg	Val	Tyr	Cys			
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Gly	Gly	Ser	Tyr	Gln	Gly	Ile	Ile	Asn	Met	Leu	Asp	Tyr	Ile	Gln	Gly			
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Met	Gly	Phe	Thr	Ala	Ile	Trp	Ile	Ser	Pro	Ile	Val	Glu	Asn	Ile	Pro			
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Asp	Asp	Thr	Gly	Tyr	Gly	Tyr	Ala	Tyr	His	Gly	Tyr	Trp	Met	Lys	Asp			
					245						250						255	
Ile	Phe	Ala	Leu	Asn	Thr	Asn	Phe	Gly	Thr	Ala	Asp	Asp	Leu	Ile	Ala			
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Leu	Ala	Thr	Glu	Leu	His	Asn	Arg	Gly	Met	Tyr	Leu	Met	Val	Asp	Ile			
					275						280						285	
Val	Val	Asn	His	Phe	Ala	Phe	Ser	Gly	Ser	His	Ala	Asp	Val	Asp	Tyr			
					290						295						300	
Ser	Glu	Tyr	Phe	Pro	Tyr	Ser	Ser	Gln	Asp	Tyr	Phe	His	Ser	Phe	Cys			
305						310						315						320

Trp Ile Thr Asp Tyr Ser Asn Gln Thr Asn Val Glu Gln Cys Trp Leu  
325 330 335

Gly Asp Asp Thr Val Pro Leu Val Asp Val Asn Thr Gln Leu Asp Thr  
340 345 350

Val Lys Ser Glu Tyr Gln Ser Trp Val Gln Glu Leu Ile Ala Asn Tyr  
355 360 365

Ser Ile Asp Gly Leu Arg Ile Asp Thr Val Lys His Val Gln Met Asp  
370 375 380

Phe Trp Ala Pro Phe Gln Glu Ala Ala Gly Ile Tyr Ala Val Gly Glu  
385 390 395 400

Val Phe Asp Gly Asp Pro Ser Tyr Thr Cys Pro Tyr Gln Glu Asn Leu  
405 410 415

Asp Gly Val Leu Asn Tyr Pro Val Tyr Tyr Pro Val Val Ser Ala Phe  
420 425 430

Glu Ser Val Ser Gly Ser Val Ser Ser Leu Val Asp Met Ile Asp Thr  
435 440 445

Leu Lys Ser Glu Cys Thr Asp Thr Thr Leu Leu Gly Ser Phe Leu Glu  
450 455 460

Asn Gln Asp Asn Pro Arg Phe Pro Ser Tyr Thr Ser Asp Glu Ser Leu  
465 470 475 480

Ile Lys Asn Ala Ile Ala Phe Thr Met Leu Ser Asp Gly Ile Pro Ile  
485 490 495

Ile Tyr Tyr Gly Gln Glu Gln Gly Leu Asn Gly Gly Asn Asp Pro Tyr  
500 505 510

Asn Arg Glu Ala Leu Trp Leu Thr Gly Tyr Ser Thr Thr Ser Thr Phe  
515 520 525

Tyr Lys Tyr Ile Ala Ser Leu Asn Gln Ile Arg Asn Gln Ala Ile Tyr  
530 535 540

Lys Asp Asp Thr Tyr Leu Thr Tyr Gln Asn Trp Val Ile Tyr Ser Asp  
545 550 555 560

Ser Thr Thr Ile Ala Met Arg Lys Gly Phe Thr Gly Asn Gln Ile Ile  
565 570 575

Thr Val Leu Ser Asn Leu Gly Thr Ser Gly Ser Ser Tyr Thr Leu Thr  
580 585 590

Leu Ser Asn Thr Gly Tyr Thr Ala Ser Ser Val Val Tyr Glu Ile Leu  
595 600 605

Thr Cys Thr Ala Val Thr Val Asp Ser Ser Gly Asn Leu Ala Val Pro  
610 615 620

Met Ser Ser Gly Leu Pro Lys Val Phe Tyr Gln Glu Ser Gln Leu Val  
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Gly Ser Gly Ile Cys Ser Met  
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<211> 1946  
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<220>  
<223> Description of Artificial Sequence: Synthetic polynucleotide  
  
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<222> (1) .. (1941)

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1 5 10 15  
  
tct cct att gtg gtt gct cgt tat att ctt cga cga gat tgc act aca 96  
Ser Pro Ile Val Val Ala Arg Tyr Ile Leu Arg Arg Asp Cys Thr Thr  
20 25 30  
  
gtt acg gtc ttg tcc tcc cct gag tct gtg acg agt tcg aac cat gtt 144  
Val Thr Val Leu Ser Ser Pro Glu Ser Val Thr Ser Ser Asn His Val  
35 40 45  
  
cag cta gcc agt cat gag atg tgc gac agt acc ttg tca gcg tcc ctt 192  
Gln Leu Ala Ser His Glu Met Cys Asp Ser Thr Leu Ser Ala Ser Leu

50	55	60	
tat atc tac aat gat gat tat gat aag att gtg aca ctt tat tat ctt			240
Tyr Ile Tyr Asn Asp Asp Tyr Asp Lys Ile Val Thr Leu Tyr Tyr Leu			
65	70	75	80
aca tcg tcg ggc aca act ggg tcc gta aca gcg tct tat tct tct agt			288
Thr Ser Ser Gly Thr Thr Gly Ser Val Thr Ala Ser Tyr Ser Ser Ser			
	85	90	95
ttg agt aac aac tgg gaa ttg tgg tct ctc tcg gct ccg gct gca gat			336
Leu Ser Asn Asn Trp Glu Leu Trp Ser Leu Ser Ala Pro Ala Ala Asp			
	100	105	110
gct gtc gag atc act gga gct agt tat gta gac agc gat gca tct gcg			384
Ala Val Glu Ile Thr Gly Ala Ser Tyr Val Asp Ser Asp Ala Ser Ala			
	115	120	125
aca tac gcc acg tct ttt gat ata cct ctt act acc acg aca acg tcg			432
Thr Tyr Ala Thr Ser Phe Asp Ile Pro Leu Thr Thr Thr Thr Thr Ser			
	130	135	140
tcg tct tct gct agt gcg act tca aca tct agt cta acc aca aca tct			480
Ser Ser Ser Ala Ser Ala Thr Ser Thr Ser Ser Leu Thr Thr Thr Ser			
145	150	155	160
agt gtt tcc att tcg gtg tcc gtc cct aca gga aca gct gca aat tgg			528
Ser Val Ser Ile Ser Val Ser Val Pro Thr Gly Thr Ala Ala Asn Trp			
	165	170	175
cga ggt agg gct atc tat cag atc gtg act gat aga ttt gca cgc act			576
Arg Gly Arg Ala Ile Tyr Gln Ile Val Thr Asp Arg Phe Ala Arg Thr			
	180	185	190
gac ggc tcc acc aca tat tta tgc gat gtt acc gat agg gtc tat tgc			624
Asp Gly Ser Thr Thr Tyr Leu Cys Asp Val Thr Asp Arg Val Tyr Cys			
	195	200	205
gga ggg tct tat cag ggg att atc aat atg ctg gat tac atc caa ggc			672
Gly Gly Ser Tyr Gln Gly Ile Ile Asn Met Leu Asp Tyr Ile Gln Gly			
	210	215	220
atg ggc ttt act gct att tgg att tct cct ata gtg gaa aat att ccc			720
Met Gly Phe Thr Ala Ile Trp Ile Ser Pro Ile Val Glu Asn Ile Pro			
225	230	235	240
gat gac acc gga tac ggt tac gca tat cat ggt tat tgg atg aaa gat			768
Asp Asp Thr Gly Tyr Gly Tyr Ala Tyr His Gly Tyr Trp Met Lys Asp			
	245	250	255
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Ile Phe Ala Leu Asn Thr Asn Phe Gly Thr Ala Asp Asp Leu Ile Ala			
	260	265	270
ttg gct acg gaa ttg cat aat cgc ggc atg tac ttg atg gtt gat att			864
Leu Ala Thr Glu Leu His Asn Arg Gly Met Tyr Leu Met Val Asp Ile			
	275	280	285

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Val Val Asn His Phe Ala Phe Ser Gly Ser His Ala Asp Val Asp Tyr	
290 295 300	
tct gaa tat ttc ccg tat tcg tcc cag gat tat ttt cat tca ttt tgc	960
Ser Glu Tyr Phe Pro Tyr Ser Ser Gln Asp Tyr Phe His Ser Phe Cys	
305 310 315 320	
tgg att aca gat tac tcg aat cag aca aac gtt gag cag tgc tgg ctt	1008
Trp Ile Thr Asp Tyr Ser Asn Gln Thr Asn Val Glu Gln Cys Trp Leu	
325 330 335	
ggc gac gat act gtt cct ctc gtg gac gtc aat acc caa ctt gac acc	1056
Gly Asp Asp Thr Val Pro Leu Val Asp Val Asn Thr Gln Leu Asp Thr	
340 345 350	
gtg aaa agt gaa tat caa tcc tgg gtt caa gaa ctt ata gct aat tac	1104
Val Lys Ser Glu Tyr Gln Ser Trp Val Gln Glu Leu Ile Ala Asn Tyr	
355 360 365	
tct att gac ggc cta aga att gac acc gtc aag cac gtg cag atg gat	1152
Ser Ile Asp Gly Leu Arg Ile Asp Thr Val Lys His Val Gln Met Asp	
370 375 380	
ttt tgg gca cca ttt caa gag gct gca ggg att tac gcc gtt ggt gaa	1200
Phe Trp Ala Pro Phe Gln Glu Ala Ala Gly Ile Tyr Ala Val Gly Glu	
385 390 395 400	
gta ttc gac ggt gat cca tcc tac aca tgt cca tat cag gaa aat ctt	1248
Val Phe Asp Gly Asp Pro Ser Tyr Thr Cys Pro Tyr Gln Glu Asn Leu	
405 410 415	
gac ggt gtc ttg aat tat cct gtt tat tat cct gtc gtc tct gcg ttt	1296
Asp Gly Val Leu Asn Tyr Pro Val Tyr Tyr Pro Val Val Ser Ala Phe	
420 425 430	
gag agt gtt agt ggg tcg gtc tcc tcg tta gtc gat atg att gat acg	1344
Glu Ser Val Ser Gly Ser Val Ser Ser Leu Val Asp Met Ile Asp Thr	
435 440 445	
ctc aag tct gaa tgc acc gac act act ctc cta ggc tcc ttt cta gag	1392
Leu Lys Ser Glu Cys Thr Asp Thr Thr Leu Leu Gly Ser Phe Leu Glu	
450 455 460	
aat caa gat aat ccg cga ttc cct agc tac act tct gat gag tct tta	1440
Asn Gln Asp Asn Pro Arg Phe Pro Ser Tyr Thr Ser Asp Glu Ser Leu	
465 470 475 480	
att aaa aat gcg atc gct ttc act atg ctc tca gac ggc att ccc ata	1488
Ile Lys Asn Ala Ile Ala Phe Thr Met Leu Ser Asp Gly Ile Pro Ile	
485 490 495	
att tat tac ggt cag gag caa ggc ctc aat ggt gga aac gat ccc tat	1536
Ile Tyr Tyr Gly Gln Glu Gln Gly Leu Asn Gly Gly Asn Asp Pro Tyr	
500 505 510	

aat cga gag gcg ctt tgg ctt acg ggc tac tcc aca acg tcg acg ttc	1584
Asn Arg Glu Ala Leu Trp Leu Thr Gly Tyr Ser Thr Thr Ser Thr Phe	
515 520 525	
tac aaa tac att gcg tcg ttg aat cag att aga aat cag gct ata tac	1632
Tyr Lys Tyr Ile Ala Ser Leu Asn Gln Ile Arg Asn Gln Ala Ile Tyr	
530 535 540	
aaa gat gat act tat ctc aca tat cag aac tgg gtt att tat tcg gat	1680
Lys Asp Asp Thr Tyr Leu Thr Tyr Gln Asn Trp Val Ile Tyr Ser Asp	
545 550 555 560	
tcc acg aca ata gca atg cgg aaa ggt ttt aca ggg aac caa ata att	1728
Ser Thr Thr Ile Ala Met Arg Lys Gly Phe Thr Gly Asn Gln Ile Ile	
565 570 575	
acg gtt ctg tca aat ctt ggg acc agt ggc agt tcg tac act ttg acg	1776
Thr Val Leu Ser Asn Leu Gly Thr Ser Gly Ser Ser Tyr Thr Leu Thr	
580 585 590	
ctt tcg aat acg gga tat acc gca tct agc gtt gta tat gag atc ttg	1824
Leu Ser Asn Thr Gly Tyr Thr Ala Ser Ser Val Val Tyr Glu Ile Leu	
595 600 605	
aca tgc aca gct gtg act gtg gat tcg tct ggg aat ttg gca gtg ccg	1872
Thr Cys Thr Ala Val Thr Val Asp Ser Ser Gly Asn Leu Ala Val Pro	
610 615 620	
atg tcc agt ggc cta cca aaa gtc ttt tat cag gaa tcg caa ctg gtt	1920
Met Ser Ser Gly Leu Pro Lys Val Phe Tyr Gln Glu Ser Gln Leu Val	
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ggc tct gga atc tgc tcc atg tagag	1946
Gly Ser Gly Ile Cys Ser Met	
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

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 <212> DNA  
 <213> Artificial Sequence

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primer

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<222> (2)..(2)  
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<212> PRT  
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peptide

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Asp Ile Val Val Asn His  
1 5

<210> 8  
<211> 6  
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<210> 9  
<211> 6  
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<211> 6  
<212> PRT  
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<210> 13  
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<212> PRT  
<213> *Pseudomonas amyloclavata*

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<210> 16  
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<212> PRT  
<213> *Klebsiella pneumoniae*

<400> 17